SEP 04

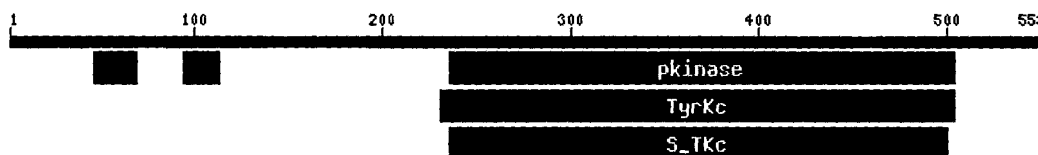1 ξ 2.

Exhibit 1

| NCBI | **CD-Search** | Entrez | ? |

RPS-BLAST 2.2.1 [Apr-13-2001]

Query=
(553 letters)

● .. This CD alignment includes 3D structure. To display structure, download **Cn3D v3.00!**

|Mouse-over boxes to display more information|

PSSMs producing significant alignments:

Score E
(bits) value

● gnl|Pfam|pfam00069 pkinase, Protein kinase domain — 180 2e-46
● gnl|Smart|smart00219 TyrKc, Tyrosine kinase, catalytic domain; Phosphotransferases.... — 161 8e-41
● gnl|Smart|smart00220 S_TKc, Serine/Threonine protein kinases, catalytic domain; Pho... — 160 2e-40
  gnl|Smart|smart00366 LRR_PS, Leucine-rich repeat, plant-specific subfamily — 38.5 0.001
  gnl|Smart|smart00366 LRR_PS, Leucine-rich repeat, plant-specific subfamily — 36.6 0.004

● gnl|Pfam|pfam00069, pkinase, Protein kinase domain.

Add query to multiple alignment, display [up to 10 ▼] sequences [most similar to the query ▼]

```
                    CD-Length = 256 residues,  97.3% aligned
                    Score =  180 bits (457), Expect = 2e-46

Query:  235  ILGRGGFGKVYKGRL-ADGSLVAVKRLKEERTPGGELQFQTEVEMISMAVHRNLLRLRGF  293
Sbjct:  6    KLGSGAFGKVYKGKHKDTGEIVAIKILKKRSLSEKKKRFLREIQILRRLSHPNIVRLLGV  65

Query:  294  CMTPTERLLVYPYMANGSVASCLRERQPSEPPLDWPTRKRIALGSARGLSYLHDHCDPKI  353
Sbjct:  66   FEEDDHLYLVMEYMEGGDLFDYLRRN---GLLLSEKEAKKIALQILRGLEYLHSR---GI  119

Query:  354  IHRDVKAANILLDEEFEAVVGDFGLARLMDYKDTHVTTAVRGTLGYIAPEYLSTGKSSEK  413
Sbjct:  120  VHRDLKPENILLDENGTVKIADFGLARKLESSSYEKLTTFVGTPEYMAPEVLEGRGYSSK  179

Query:  414  TDVFGYGIMLLELITGQRAFDLARLANDDDVMLLDWVKSLLKEKKLEMLVDPDLENNYID  473
Sbjct:  180  VDVWSLGVILYELLTGKLPFP--GIDPLEELFRIKE-------------RPRLRLPLPP  223

Query:  474  TEVEQLIQVALLCTQGSPMERPKMSEVVRML  504
Sbjct:  224  NCSEELKDLIKKCLNKDPEKRPTAKEILNHP  254
```

http://www.ncbi.nlm.nih.gov/Structure/cdd/qrpsb.cgi?RID=999266785-25747-32142   8/31/2001

gnl|Smart|smart00219, TyrKc, Tyrosine kinase, catalytic domain; Phosphotransferases. Tyrosine-specific kinase subfamily.

Add query to multiple alignment, display `up to 10 ▼` sequences `most similar to the query ▼`

```
          CD-Length = 258 residues,  99.6% aligned
          Score =  161 bits (408), Expect = 8e-41

Query:  231  TFSTILGRGGFGKVYKGRLADGS----LVAVKRLKEERTPGGELQFQTEVEMISMAVHRN  286
Sbjct:    2  TLGKKLGEGAFGEVYKGTLKGKGGVEVEVAVKTLKEDASEQQIEEFLREARLMRKLDHPN   61

Query:  287  LLRLRGFCMTPTERLLVYPYMANGSVASCLRERQPSEPPLDWPTRKRIALGSARGLSYLH  346
Sbjct:   62  IVKLLGVCTEEEPLMIVMEYMEGGDLLDYLRKNRPKE--LSLSDLLSFALQIARGMEYLE  119

Query:  347  DHCDPKIIHRDVKAANILLDEEFEAVVGDFGLARLMDYKDTHVTTAVRGT-LGYIAPEYL  405
Sbjct:  120  SK---NFVHRDLAARNCLVGENKTVKIADFGLARDLYDDDYYRKKKSPRLPIRWMAPESL  176

Query:  406  STGKSSEKTDVFGYGIMLLELIT-GQRAFDLARLANDDDVMLLDWVKSLLKEKKLEMLVD  464
Sbjct:  177  KDGKFTSKSDVWSFGVLLWEIFTLGESPY--PGMSNEE-------------------VL  214

Query:  465  PDLENNY----IDTEVEQLIQVALLCTQGSPMERPKMSEVVRML  504
Sbjct:  215  EYLKKGYRLPQPPNCPDEIYDLMLQCWAEDPEDRPTFSELVERL  258
```

● gnl|Smart|smart00220, S_TKc, Serine/Threonine protein kinases, catalytic domain; Phosphotransferases. Serine or threonine-specific kinase subfamily.

Add query to multiple alignment, display `up to 10 ▼` sequences `most similar to the query ▼`

```
          CD-Length = 256 residues,  95.7% aligned
          Score =  160 bits (405), Expect = 2e-40

Query:  235  ILGRGGFGKVYKGR-LADGSLVAVKRLKEERTPGGELQ-FQTEVEMISMAVHRNLLRLRG  292
Sbjct:    6  VLGKGAFGKVYLARDKKTGKLVAIKVIKKEKLKKKKRERILREIKILKKLDHPNIVKLYD   65

Query:  293  FCMTPTERLLVYPYMANGSVASCLRERQPSEPPLDWPTRKRIALGSARGLSYLHDHCDPK  352
Sbjct:   66  VFEDDDKLYLVMEYCEGGDLFDLLKKR----GRLSEDEARFYARQILSALEYLHSQ---G  118

Query:  353  IIHRDVKAANILLDEEFEAVVGDFGLARLMDYKDTHVTTAVRGTLGYIAPEYLSTGKSSE  412
Sbjct:  119  IIHRDLKPENILLDSDGHVKLADFGLAKQLDSGGTLLTTFV-GTPEYMAPEVLLGKGYGK  177

Query:  413  KTDVFGYGIMLLELITGQRAFDLARLANDDDVMLLDWVKSLLKEKKLEMLVDPDLENNYI  472
Sbjct:  178  AVDIWSLGVILYELLTGKPPFP----GDDQLLALFKKI--------GKPPPPFPPPEWKI  225

Query:  473  DTEVEQLIQVALLCTQGSPMERPKMSEV  500
Sbjct:  226  SPEAKDLIK---KLLVKDPEKRLTAEEA  250
```

gnl|Smart|smart00366, LRR_PS, Leucine-rich repeat, plant-specific subfamily

Add query to multiple alignment, display `up to 10 ▼` sequences `most similar to the query ▼`

```
          CD-Length = 24 residues, 100.0% aligned
          Score = 38.5 bits (88), Expect = 0.001
```

```
Query:  46   LTNLVSLDLYMNSFSGPIPDTLGK   69
Sbjct:   1   LTSLQVLDLSNNNLSGEIPESLGN   24
```

gnl|Smart|smart00366, LRR_PS, Leucine-rich repeat, plant-specific subfamily

Add query to multiple alignment, display [up to 10 ▼] sequences [most similar to the query ▼]

CD-Length = 24 residues, 83.3% aligned
Score = 36.6 bits (83), Expect = 0.004

```
Query:  94   ITTLQVLDLSNNRLSGPVPD   113
Sbjct:   1   LTSLQVLDLSNNNLSGEIPE    20
```

32

```
┌──────┐                                    ┌────────┐ ┌─┐
│ NCBI │          CD-Search                 │ Entrez │ │?│
└──────┘                                    └────────┘ └─┘
```
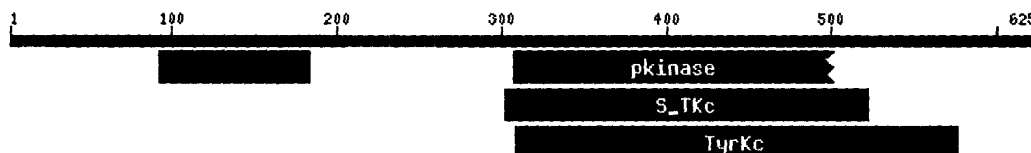
RPS-BLAST 2.2.1 [Apr-13-2001]

Query=
(625 letters)

● .. This CD alignment includes 3D structure. To display structure, download **Cn3D v3.00**!

Mouse-over boxes to display more information

```
1      100      200      300      400      500      625

                                        pkinase
                                         S_TKc
                                         TyrKc
```

PSSMs producing significant alignments:	Score (bits)	E value

● gnl|Pfam|pfam00069   pkinase, Protein kinase domain   177   2e-45

● gnl|Smart|smart00220 S_TKc, Serine/Threonine protein kinases, catalytic domain; Pho...   160   1e-40

● gnl|Smart|smart00219 TyrKc, Tyrosine kinase, catalytic domain; Phosphotransferases....   156   3e-39

   gnl|Smart|smart00366 LRR_PS, Leucine-rich repeat, plant-specific subfamily   39.3   6e-04

   gnl|Smart|smart00366 LRR_PS, Leucine-rich repeat, plant-specific subfamily   38.1   0.001

   gnl|Smart|smart00366 LRR_PS, Leucine-rich repeat, plant-specific subfamily   37.7   0.002

   gnl|Smart|smart00366 LRR_PS, Leucine-rich repeat, plant-specific subfamily   35.4   0.009

● gnl|Pfam|pfam00069, pkinase, Protein kinase domain.

Add query to multiple alignment, display [up to 10 ▼] sequences [most similar to the query ▼]

```
            CD-Length = 256 residues, only  74.6% aligned
            Score =  177 bits (449), Expect = 2e-45

Query:  307  ILGRGGFGKVYKGRL-ADGTLVAVKRLKEERTPGGELQFQTEVEMISMAVHRNLLRLRGF  365
Sbjct:  6    KLGSGAFGKVYKGKHKDTGEIVAIKILKKRSLSEKKKRFLREIQILRRLSHPNIVRLLGV  65

Query:  366  CMTPTERLLVYPYMANGSVASCLRERPPSQPPLDWPTRKRIALGSARGLSYLHDHCDPKI  425
Sbjct:  66   FEEDDHLYLVMEYMEGGDLFDYLRRNGL---LLSEKEAKKIALQILRGLEYLHSR---GI  119

Query:  426  IHRDVKAANILLDEEFEAVVGDFGLAKLMDYKDTHVTTAVRGTIGHIAPEYLSTGKSSEK  485
Sbjct:  120  VHRDLKPENILLDENGTVKIADFGLARKLESSSYEKLTTFVGTPEYMAPEVLEGRGYSSK  179

Query:  486  TDVFGYGIMLLELITGQ  502
Sbjct:  180  VDVWSLGVILYELLTGK  196
```

---

gnl|Smart|smart00220, S_TKc, Serine/Threonine protein kinases, catalytic domain;
Phosphotransferases. Serine or threonine-specific kinase subfamily.

Add query to multiple alignment, display `up to 10 ▼` sequences `most similar to the query          ▼`

```
        CD-Length = 256 residues,  82.4% aligned
        Score =  160 bits (406), Expect = 1e-40

Query:  302  FSNKNILGRGGFGKVYKGR-LADGTLVAVKRL-KEERTPGGELQFQTEVEMISMAVHRNL  359
Sbjct:  1    YELLEVLGKGAFGKVYLARDKKTGKLVAIKVIKKEKLKKKKRERILREIKILKKLDHPNI  60

Query:  360  LRLRGFCMTPTERLLVYPYMANGSVASCLRERPPSQPPLDWPTRKRIALGSARGLSYLHD  419
Sbjct:  61   VKLYDVFEDDDKLYLVMEYCEGGDLFDLLKKRGR----LSEDEARFYARQILSALEYLHS  116

Query:  420  HCDPKIIHRDVKAANILLDEEFEAVVGDFGLAKLMDYKDTHVTTAVRGTIGHIAPEYLST  479
Sbjct:  117  Q---GIIHRDLKPENILLDSDGHVKLADFGLAKQLDSGGTLLTTFV-GTPEYMAPEVLLG  172

Query:  480  GKSSEKTDVFGYGIMLLELITGQRAFDLARLANDDDVMLLDWV  522
Sbjct:  173  KGYGKAVDIWSLGVILYELLTGKPPFP----GDDQLLALFKKI  211
```

● gnl|Smart|smart00219, TyrKc, Tyrosine kinase, catalytic domain; Phosphotransferases. Tyrosine-
specific kinase subfamily.

Add query to multiple alignment, display `up to 10 ▼` sequences `most similar to the query          ▼`

```
        CD-Length = 258 residues,  97.7% aligned
        Score =  156 bits (395), Expect = 3e-39

Query:  308  LGRGGFGKVYKGRLADG----TLVAVKRLKEERTPGGELQFQTEVEMISMAVHRNLLRLR  363
Sbjct:  7    LGEGAFGEVYKGTLKGKGGVEVEVAVKTLKEDASEQQIEEFLREARLMRKLDHPNIVKLL  66

Query:  364  GFCMTPTERLLVYPYMANGSVASCLRERPPSQPPLDWPTRKRIALGSARGLSYLHDHCDP  423
Sbjct:  67   GVCTEEEPLMIVMEYMEGGDLLDYLRKNRP--KELSLSDLLSFALQIARGMEYLESK---  121

Query:  424  KIIHRDVKAANILLDEEFEAVVGDFGLAKLMDYKDTHVTTAVRGT-IGHIAPEYLSTGKS  482
Sbjct:  122  NFVHRDLAARNCLVGENKTVKIADFGLARDLYDDDYYRKKKSPRLPIRWMAPESLKDGKF  181

Query:  483  SEKTDVFGYGIMLLELIT-GQRAFDLARLANDDDVMLLDWVKGLLKEKKLEMLVDPDLQT  541
Sbjct:  182  TSKSDVWSFGVLLWEIFTLGESPY-----PGMSNEEVLEYLKKGYRLPQPPNCPDE----  232

Query:  542  NYEERELEQVIQVALLCTQGSPMERPKMSEVVRML  576
Sbjct:  233  ---------IYDLMLQCWAEDPEDRPTFSELVERL  258
```

gnl|Smart|smart00366, LRR_PS, Leucine-rich repeat, plant-specific subfamily

Add query to multiple alignment, display `up to 10 ▼` sequences `most similar to the query          ▼`

```
        CD-Length = 24 residues, 100.0% aligned
        Score = 39.3 bits (90), Expect = 6e-04

Query:  92  LKNLQYLELYSNNITGPIPSNLGN  115
Sbjct:  1   LTSLQVLDLSNNNLSGEIPESLGN  24
```

---

gnl|Smart|smart00366, LRR_PS, Leucine-rich repeat, plant-specific subfamily

__Add__ query to multiple alignment, display | up to 10 ▼ | sequences | most similar to the query ▼ |

```
        CD-Length = 24 residues, 100.0% aligned
        Score = 38.1 bits (87), Expect = 0.001

Query:  116  LTNLVSLDLYLNSFSGPIPESLGK  139
Sbjct:  1    LTSLQVLDLSNNNLSGEIPESLGN  24
```

---

gnl|Smart|smart00366, LRR_PS, Leucine-rich repeat, plant-specific subfamily

__Add__ query to multiple alignment, display | up to 10 ▼ | sequences | most similar to the query ▼ |

```
        CD-Length = 24 residues, 100.0% aligned
        Score = 37.7 bits (86), Expect = 0.002

Query:  140  LSKLRFLRLNNNSLTGSIPMSLTN  163
Sbjct:  1    LTSLQVLDLSNNNLSGEIPESLGN  24
```

---

gnl|Smart|smart00366, LRR_PS, Leucine-rich repeat, plant-specific subfamily

__Add__ query to multiple alignment, display | up to 10 ▼ | sequences | most similar to the query ▼ |

```
        CD-Length = 24 residues,  83.3% aligned
        Score = 35.4 bits (80), Expect = 0.009

Query:  164  ITTLQVLDLSNNRLSGSVPD  183
Sbjct:  1    LTSLQVLDLSNNNLSGEIPE  20
```

.../qrpsb.cgi?RID=999267729-8513-4292&GRAPH=2&PAIR=2&EXPECT=0.010000&NHIT 8/31/2001

Exhibit 3

Molecule: 32   NoName,   2072 bps DNA
Description:
File Name: seq id 32.cm5,   dated 31 Aug 2001
Printed: 195-2072 bps,   format Translated, Frame 3

```
195    atggagtcga gttatgtggt gtttatctta ctttcactga tcttacttcc
        M  E  S   S  Y  V   V  F  I  L   L  S  L   I  L  L

245    gaatcattca ctgtggcttg cttctgctaa tttggaaggt gatgctttgc
        P  N  H  S   L  W  L   A  S  A   N  L  E  G   D  A  L

295    atactttgag ggttactcta gttgatccaa acaatgtctt gcagagctgg
        H  T  L   R  V  T  L   V  D  P   N  N  V   L  Q  S  W

345    gatcctacgc tagtgaatcc ttgcacatgg ttccatgtca cttgcaacaa
        D  P  T   L  V  N   P  C  T  W   F  H  V   T  C  N

395    cgagaacagt gtcataagag ttgatttggg gaatgcagag ttatctggcc
        N  E  N  S   V  I  R   V  D  L   G  N  A  E   L  S  G

445    atttagttcc agagcttggt gtgctcaaga atttgcagta tttggagctt
        H  L  V   P  E  L  G   V  L  K   N  L  Q   Y  L  E  L

495    tacagtaaca acataactgg cccgattcct agtaatcttg gaaatctgac
        Y  S  N   N  I  T   G  P  I  P   S  N  L   G  N  L

545    aaacttagtg agtttggatc tttacttaaa cagcttctcc ggtcctattc
        T  N  L  V   S  L  D   L  Y  L   N  S  F  S   G  P  I

595    cggaatcatt gggaaagctt tcaaagctga gatttctccg gcttaacaac
        P  E  S   L  G  K  L   S  K  L   R  F  L   R  L  N  N

645    aacagtctca ctgggtcaat tcctatgtca ctgaccaata ttactaccct
        N  S  L   T  G  S   I  P  M  S   L  T  N   I  T  T

695    tcaagtgtta gatctatcaa ataacagact ctctggttca gttcctgaca
        L  Q  V  L   D  L  S   N  N  R   L  S  G  S   V  P  D

745    atggctcctt ctcactcttc acacccatca gttttgctaa taacttagac
        N  G  S   F  S  L  F   T  P  I   S  F  A   N  N  L  D

795    ctatgtggac ctgttacaag tcacccatgt cctggatctc ccccgttttc
        L  C  G   P  V  T   S  H  P  C   P  G  S   P  P  F

845    tcctccacca ccttttattc aacctccccc agtttccacc ccgagtgggt
        S  P  P   P  F  I   Q  P  P   P  V  S  T   P  S  G

895    atggtataac tggagcaata gctggtggag ttgctgcagg tgctgctttg
        Y  G  I   T  G  A  I   A  G  G   V  A  A   G  A  A  L

945    ccctttgctg ctcctgcaat agcctttgct tggtggcgac gaagaagccc
        P  F  A   A  P  A   I  A  F  A   W  W  R   R  R  S
```

```
995    actagatatt ttcttcgatg tccctgccga agaagatcca gaagttcatc
       P L D I    F F D    V P A    E E D P    E V H

1045   tgggacagct caagaggttt tctttgcggg agctacaagt ggcgagtgat
       L G Q    L K R F    S L R    E L Q    V A S D

1095   gggtttagta acaagaacat tttgggcaga ggtgggtttg ggaaagtcta
       G F S    N K N    I L G R    G G F    G K V

1145   caagggacgc ttggcagacg gaactcttgt tgctgtcaag agactgaagg
       Y K G R    L A D    G T L    V A V K    R L K

1195   aagagcgaac tccaggtgga gagctccagt ttcaaacaga agtagagatg
       E E R    T P G G    E L Q    F Q T    E V E M

1245   ataagtatgg cagttcatcg aaacctgttg agattacgag gtttctgtat
       I S M    A V H    R N L L    R L R    G F C

1295   gacaccgacc gagagattgc ttgtgtatcc ttacatggcc aatggaagtg
       M T P T    E R L    L V Y    P Y M A    N G S

1345   ttgcttcgtg tctcagagag aggccaccgt cacaacctcc gcttgattgg
       V A S    C L R E    R P P    S Q P    P L D W

1395   ccaacgcgga agagaatcgc gctaggctca gctcgaggtt tgtcttacct
       P T R    K R I    A L G S    A R G    L S Y

1445   acatgatcac tgcgatccga agatcattca ccgtgacgta aaagcagcaa
       L H D H    C D P    K I I    H R D V    K A A

1495   acatcctctt agacgaagaa ttcgaagcgg ttgttggaga tttcgggttg
       N I L    L D E E    F E A    V V G    D F G L

1545   gcaaagctta tggactataa agacactcac gtgacaacag cagtccgtgg
       A K L    M D Y    K D T H    V T T    A V R

1595   caccatcggt cacatcgctc cagaatatct ctcaaccgga aaatcttcag
       G T I G    H I A    P E Y    L S T G    K S S

1645   agaaaaccga cgttttcgga tacggaatca tgcttctaga actaatcaca
       E K T    D V F G    Y G I    M L L    E L I T

1695   ggacaaagag ctttcgatct cgctcggcta gctaacgacg acgacgtcat
       G Q R    A F D    L A R L    A N D    D D V

1745   gttacttgac tgggtgaaag gattgttgaa ggagaagaag ctagagatgt
       M L L D    W V K    G L L    K E K K    L E M

1795   tagtggatcc agatcttcaa acaaactacg aggagagaga actggaacaa
       L V D    P D L Q    T N Y    E E R    E L E Q

1845   gtgatacaag tggcgttgct atgcacgcaa ggatcaccaa tggaaagacc
       V I Q    V A L    L C T Q    G S P    M E R
```

KINASE
DOMAIN
SEQ ID
NO 32

NoName 32

```
1895   aaagatgtct gaagttgtaa ggatgctgga aggagatggg cttgcggaga
        P   K   M   S   E   V   V   R   M   L   E   G   D   G   L   A   E

1945   aatgggacga atggcaaaaa gttgagattt tgagggaaga gattgatttg
        K   W   D   E   W   Q   K   V   E   I   L   R   E   E   I   D   L

1995   agtcctaatc ctaactctga ttggattctt gattctactt acaatttgca
        S   P   N   P   N   S   D   W   I   L   D   S   T   Y   N   L

2045   cgccgttgag ttatctggtc caaggtaa
        H   A   V   E   L   S   G   P   R   -
```

Reference molecule: NoName   1020 - 1684   (665 bps) Homology

        Sequence 2:   NoName   3304 - 4081   (778 bps)   100%

Alignment type: Local (FastScan)
Homology details: Percent Max 78; Score 522; Length 665

NoName 32   (1020) gccgaagaagatccagaagttcatctgggacagctcaagagggttttctttgcgggagcta
NoName 20   (3304) ....

NoName   (1080) caagtggcgagtgatgggtttagtaacaagaacatttttgggcagaggtgggtttgggaaa
NoName   (3364) ....

NoName   (1140) rgtctacaagggacgcttggcagacggaactcttgttgctgtcaagagactgaaggaagag
NoName   (3424) ....

NoName   (1200) cgaactccaggtggagagctccagtttcaaacagaagtagagatgataagtatggcagtt
NoName   (3484) ....

NoName   (1260) catcgaaacctgttgagattacgaggtttctgtatgacaccgaccgagagattgcttgtg
NoName   (3544) ....

NoName   (1320) tatccttacatggccaatggaagtgttgcttcgtgtctcagag-----------------
NoName   (3604) ....gtaaaaactaaacaatt

NoName   (1363) --
NoName   (3664) aaacatcttgtgctctctctcaattactttgacgtgaagtgtttttttcatgttttccttt

NoName   (1363) ---------------------------------agaggccaccgtcacaacctccgc
NoName   (3724) atgggttcataattgttggttacactaatgacacag......................

NoName   (1387) ttgattggccaacgcggaagagaatcgcgctaggctcagctcgaggtttgtcttacctac
NoName   (3784) ....

NoName   (1447) atgatcactgcgatccgaagatcattcaccgtgacgtaaaagcagcaaacatcctcttag
NoName   (3844) ....

NoName   (1507) acgaagaattcgaagcggttgttggagatttcgggttggcaaagcttatggactataaag
NoName   (3904) ....a...........

NoName   (1567) acactcacgtgacaacagcagtccgtggcaccatcggtcacatcgctccagaatatctct
NoName   (3964) ....

NoName   (1627) caaccggaaaatcttcagagaaaaccgacgttttcggatacggaatcatgcttctaga
NoName   (4024) ....